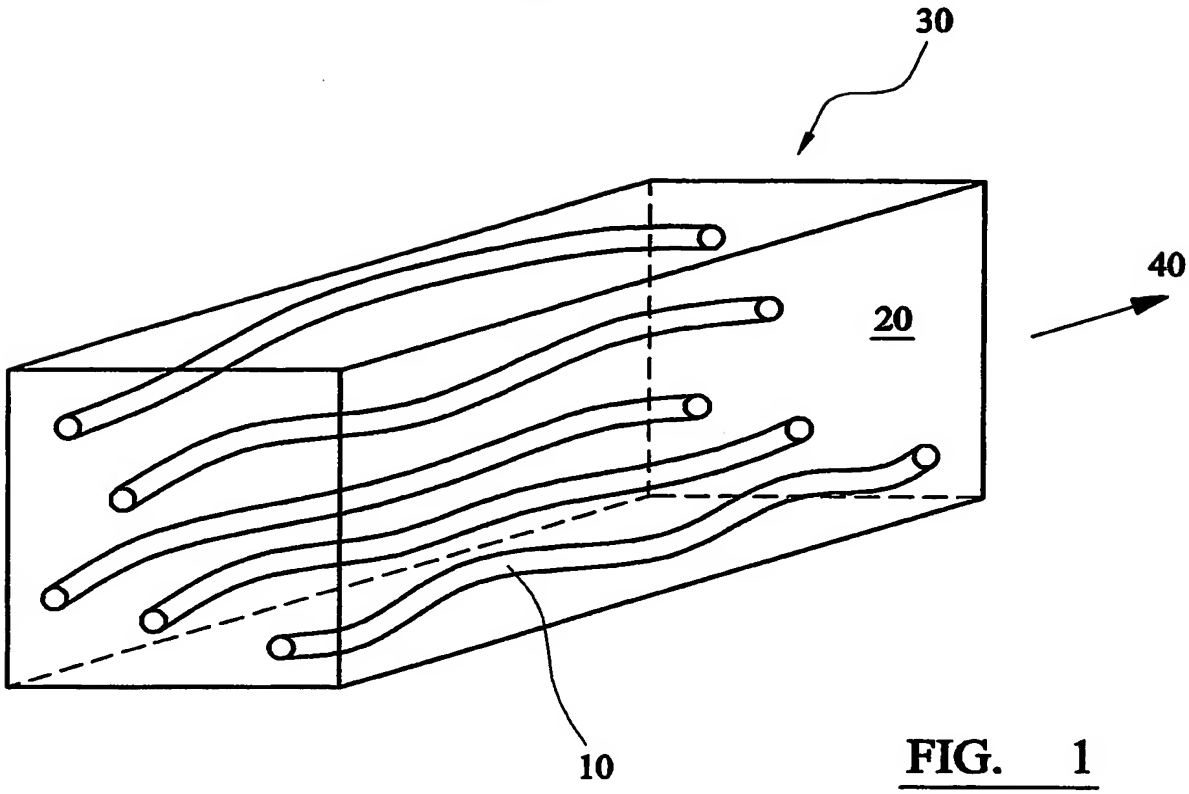


FIG. 1

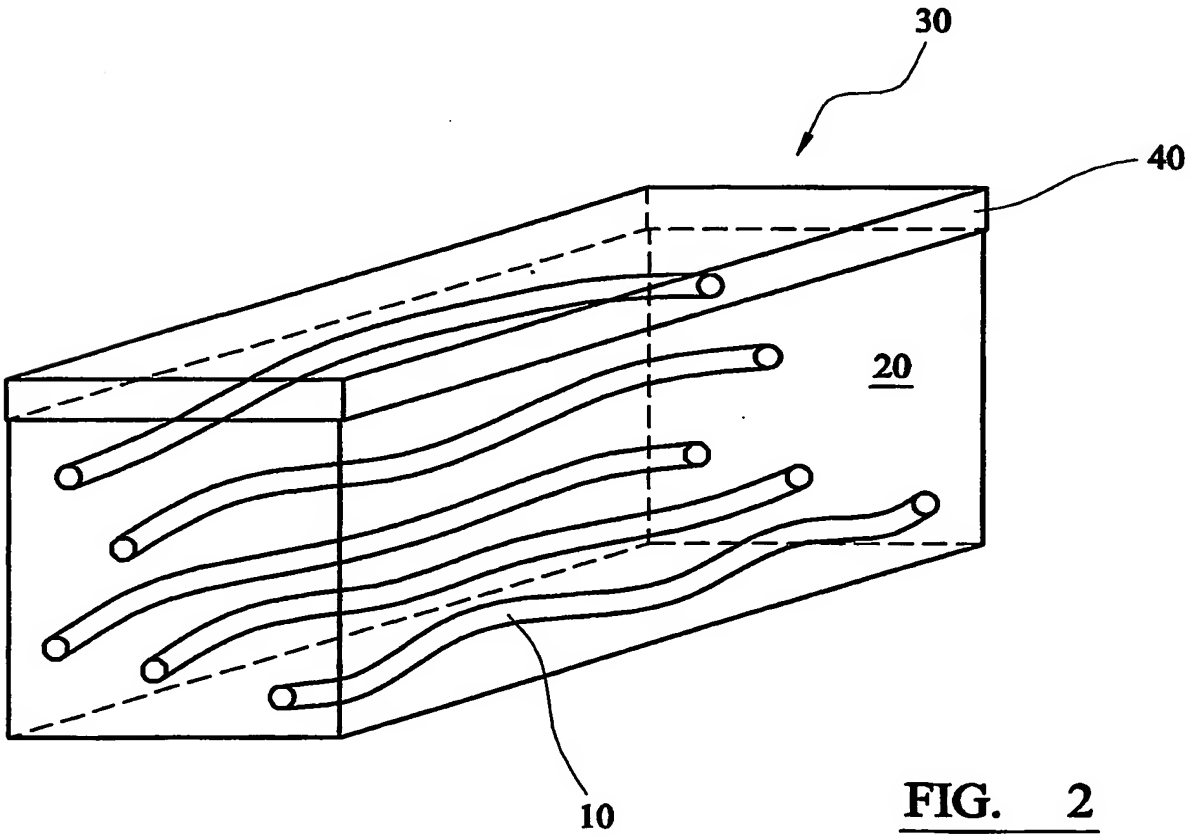


FIG. 2

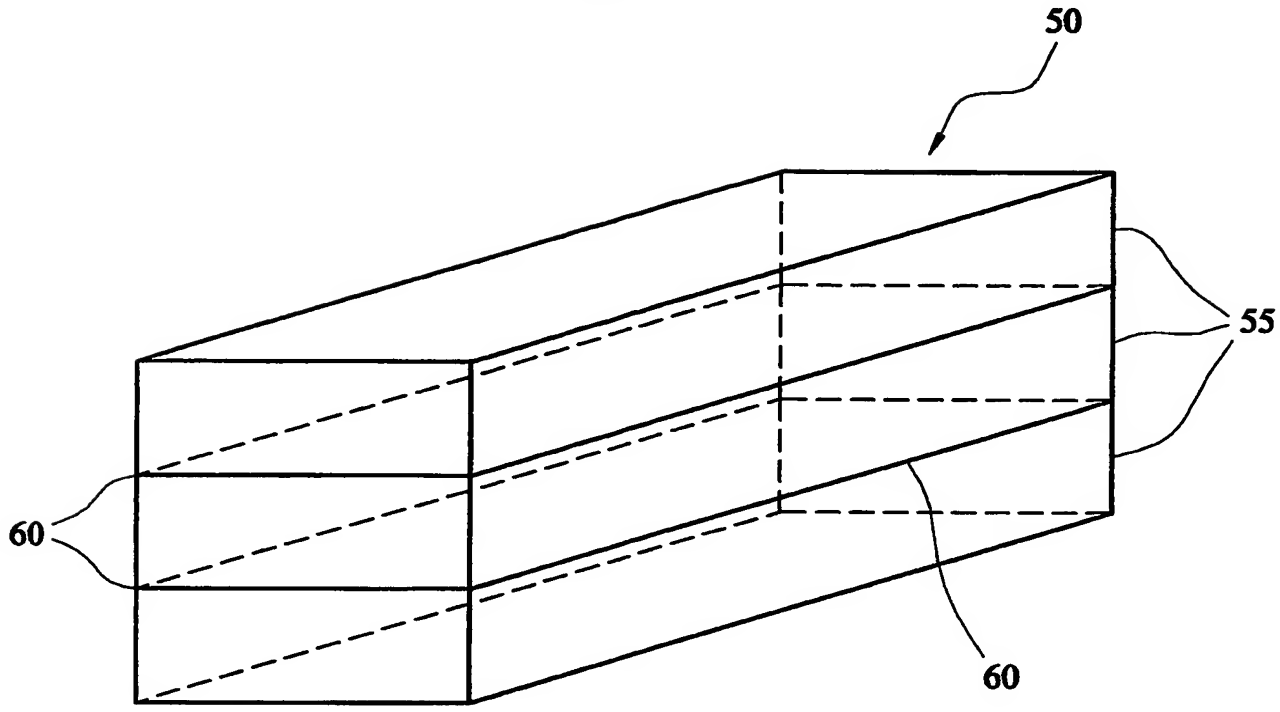


FIG. 3

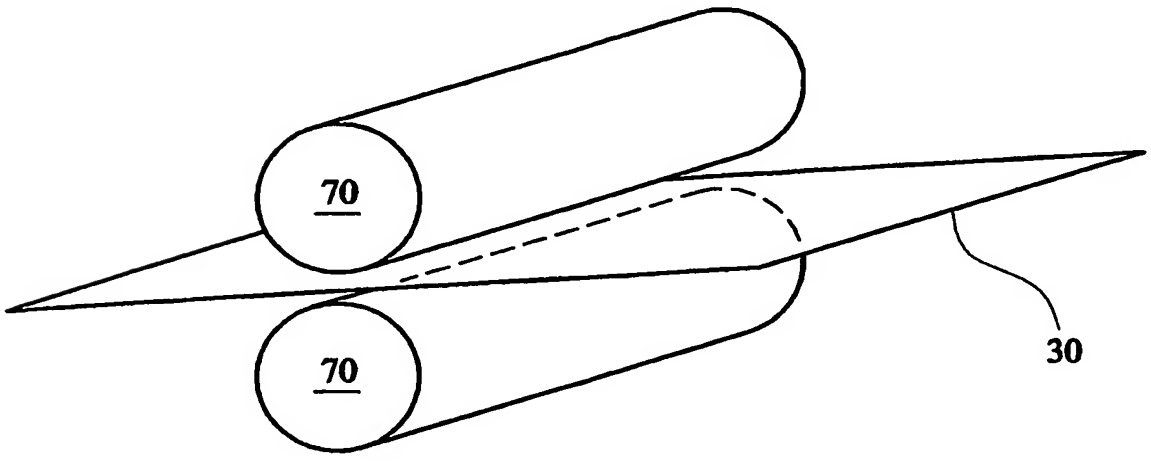


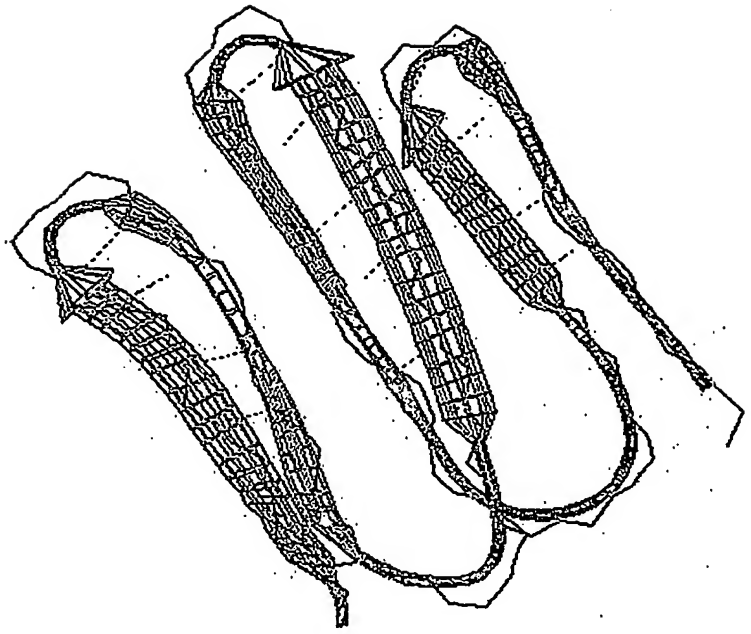
FIG. 4

Consenus repeat structure of sericin precureor protein

No. of Repeats	Total Score	Length	Diagonal	BW-From	BW-To	Level
7	529.97	35	35	317	351	1

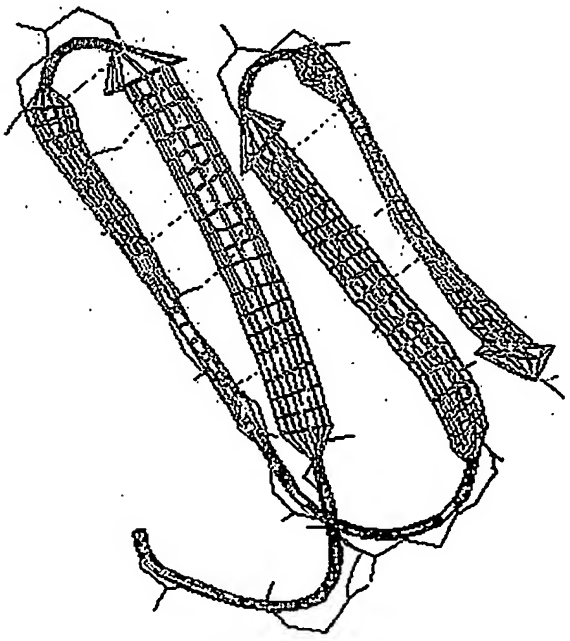
```
  131-  164 (46.31/ 7.35)   SSSSSSTeeSS....SSSSR..AASSTDASSNTDSNSNSA
  165-  202 (82.44/20.60)   GSSTSGG..RRTYGYSSNSRDGSVSSTGSSSNTDSNSSNA
  203-  240 (83.27/20.91)   GSSTSGG..SSTYGYSSNSRDGSVSTTGSSSNTDSNSNSV
  241-  278 (68.12/15.35)   GSRRSGG..SSSHSDSSKSRDSNVSTTGSSSNTDSNSNSV
  279-  316 (82.44/20.60)   GSSTSGG..RRTYGYSSNSRDGSVSSTGSSSNTDSNSNSV
  317-  354 (84.15/21.23)   GSSTSGG..SSTYGYSSNSRDGSVSSTGSSSNTDSNSNSA
  355-  389 (83.23/20.90    GSSTSGG..SSTYGYSSNSHDGSVSSTGSSSNTDSNS
```

FIG. 5



Ice nucleation protien (inaz) from the published PDB file

FIG. 6



Swiss model for consensus sequence of sericin precursor protein using inaz as a template

FIG. 7

The best LALIGN alignment of sericin precursor protein with INAC.

```
24.4% identity in 336 aa overlap; score: 265 E(10,000): 4.9e-16

     500       510       520       530       540       550
INAZ  STGTAGADSSLIAGYGSTQTSGSESSLTAGYGSTQTAREGSTLTAGYGSTGTAGADSSLI
      :.:.  : :   .   :  ::: :.  :.: ...    . . ...:  :...   ..
serici SAGAHRAKSVEQSQDKSKYTSGPEGVSTSGRSQNYKDSKQAIISGGTKSSNSNVQSDEKS
           60        70        80        90       100       110

     560       570       580       590       600       610
INAZ  AGYGSTQTSGSESSLTAGYGSTQTAQQGSVLTSGYGSTQTAGAASNLTTGYGSTGTAGHE
      :. .:.. :..::.  .. .:..: ...:  . . .::.... ... ... ::. ..:..
serici ASQSSSSRSSQESASYSSSSSSSTEESSSSSSRAASSTDASSNTDSNSNSAGSSTSGGRR
          120       130       140       150       160       170

     620       630       640       650       660       670
INAZ  SFIIAGY---GSTQTAGHKSILTAGYGSTQTARDGSDLIAGYGSTGTAGS----GSSLIA
      ..  ..    ::....: .:   .. ... .. .:..   ::.:..  ::    :::  .
serici TYGYSSNSRDGSVSSTGSSSNTDSNSSNAGSSTSGGSSTYGYSSNSRDGSVSTTGSSSNT
          180       190       200       210       220       230

          680       690       700       710       720       730
INAZ  GYGSTQTASYRSMLTAGYGSTQTAREHSDLVTGYGSTSTAGSNSSLIAGYGSTQTAGFKS
       .:....: ::  .... ... .:...  .:: .:.. ..:::   .  :. .: :..:
serici DSNSNSVGSRRSGGSSSHEDSSKSRDENVSTTGSSSNTDSNSNSVGSSTSGGRRTYGYSS
          240       250       260       270       280       290
```

FIG. 8